

SEQUENCE LISTING

<110> Garcia-Martinez, Leon Fernando
 Chen, Yuching
 Andrews, Dawn
 Celltech R&D, Inc.

<120> Modulating Immune Responses

<130> 1427.008US1

<160> 99

<170> FastSEQ for Windows Version 4.0

<210> 1
 <211> 2051
 <212> DNA
 <213> Mus musculus

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<210> 2
 <211> 196
 <212> PRT
 <213> Mus musculus

<400> 2

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<210> 3
<211> 2051
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic mutant CD83 sequence

<400> 3

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<210> 4
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<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic mutant CD83 sequence

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Ala Asp Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Leu	Ser Tyr Ala					
35	40	45				
Val Ser Trp Ala Lys Val Ser Glu Ser Gly Thr Glu Ser	Val Glu Leu					
50	55	60				
Pro Glu Ser Lys Gln Asn Ser Ser Phe Glu Ala Pro Arg	Arg Arg Ala					
65	70	75	80			
Tyr Ser Leu Thr Ile Gln Asn Thr Thr Ile Cys Ser Ser	Gly Thr Tyr					
85	90	95				
Arg Cys Ala Leu Gln Glu Leu Gly Gly Gln Arg Asn Leu	Ser Gly Thr					
100	105	110				
Val Val Leu Lys Val Thr Gly Cys Pro Lys Glu Ala Thr	Glu Ser Thr					
115	120	125				
Phe Arg Lys Tyr Arg Ala Glu Ala Val Leu Leu Phe Ser	Leu Val Val					
130	135	140				
Phe Tyr Leu Thr Leu Ile Ile Phe Thr Cys Lys Phe Ala Arg	Leu Gln					
145	150	155	160			
Ser Ile Phe Pro Asp Ile Ser Lys Pro Gly Thr Glu Gln	Ala Phe Leu					
165	170	175				
Pro Val Thr Ser Pro Ser Lys His Leu Gly Pro Val Thr Leu	Pro Lys					
180	185	190				
Thr Glu Thr Val Arg Val Gly Ser Pro Leu Val Phe Thr	Lys Pro Arg					
195	200	205				
Ala His Gln Ile Ser Val Pro Glu Cys His Pro Asp Lys	Arg Arg Met					
210	215	220				
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Val Gly Ser Thr Leu Leu Pro Asp Thr Gly Ser						
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<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic mutant CD83 sequence

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<210> 6

<400> 6
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<210> 7
<211> 168
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic mutant CD83 sequence

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<210> 8
<211> 55
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic mutant CD83 sequence

<400> 8
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Ser Val Pro Glu Cys His Pro Asp Lys Arg Arg Met Ser Ser Ile Leu
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Arg Trp Gln Pro Phe Phe Glu Val Leu His Leu Thr Val Gly Ser Thr
35 40 45
Leu Leu Pro Asp Thr Gly Ser
50 55

<210> 9
<211> 205
<212> PRT
<213> Homo sapiens

<400> 9
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20 25 30

Leu Pro Cys Thr Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser
 35 40 45
 Trp Val Lys Leu Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln
 50 55 60
 Glu Asp His Leu Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly
 65 70 75 80
 Ser Phe Asp Ala Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn
 85 90 95
 Thr Thr Ser Cys Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro
 100 105 110
 Asp Gly Gln Arg Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr Gly
 115 120 125
 Cys Pro Ala Gln Arg Lys Glu Glu Thr Phe Lys Lys Tyr Arg Ala Glu
 130 135 140
 Ile Val Leu Leu Ala Leu Val Ile Phe Tyr Leu Thr Leu Ile Ile
 145 150 155 160
 Phe Thr Cys Lys Phe Ala Arg Leu Gln Ser Ile Phe Pro Asp Phe Ser
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 Lys Ala Gly Met Glu Arg Ala Phe Leu Pro Val Thr Ser Pro Asn Lys
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 His Leu Gly Leu Val Thr Pro His Lys Thr Glu Leu Val
 195 200 205

<210> 10
 <211> 2574
 <212> DNA
 <213> Homo sapiens

<400> 10

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<211> 239
<212> PRT
<213> Artificial Sequence
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<220>
<223> A synthetic 20D04 light chain sequence

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      20          25          30
Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala
      35          40          45
Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
      50          55          60
Gln Pro Pro Lys Leu Leu Ile Tyr Arg Thr Ser Thr Leu Ala Ser Gly
      65          70          75          80
Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu
      85          90          95
Thr Ile Ser Gly Val Gln Cys Asp Asp Val Ala Thr Tyr Tyr Cys Gln
      100         105         110
Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala Phe Gly Gly
      115         120         125
Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
      130         135         140
Leu Phe Pro Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile
      145         150         155         160
Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu
      165         170         175
Val Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro
      180         185         190
Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
      195         200         205
Thr Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr
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Gln Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
      225         230         235

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<211> 720
<212> DNA
<213> Artificial Sequence
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<220>
<223> A synthetic 20D04 anti-CD83 light chain sequence

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acagtccatcca	tcaattgccaa	ggccagtgaa	agcattagca	actacttata	ctggtatcag	180
cagaaccagg	ggcagccctcc	caagctcctg	atctacagga	catccactct	ggcatctggg	240
gtctcatcg	ggttcaaagg	cagtggatct	gggacagagt	acactctcac	catcagcggc	300
gtgcagtgt	acgatgtgc	cacttactac	tgtcaatgca	cttctgggtgg	gaagttcatt	360
agtatggtg	ctgcttcgg	cggagggacc	gaggtgggtgg	tcaaaggta	tccagttgca	420
cctactgtcc	tcctttccc	accatctac	gatgaggtgg	caactggAAC	agtaccatc	480
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acccaaacaa	ctggcatcga	gaacagtaaa	acaccgcaga	attctgcaga	ttgtacctac	600
aacctcagca	gcactctgac	actgaccagc	acacagtaca	acagccacaa	agagtacacc	660
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<210> 13
<211> 454
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic 20D04 heavy chain sequence

<400> 13																			
Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly				
1				5				10					15						
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro				
					20				25				30						
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Ser	Leu	Ser				
						35			40			45							
Asn	Asn	Ala	Ile	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu				
						50			55			60							
Trp	Ile	Gly	Tyr	Ile	Trp	Ser	Gly	Gly	Leu	Thr	Tyr	Tyr	Tyr	Ala	Asn	Trp			
						65			70			75				80			
Ala	Glu	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu				
						85			90			95							
Lys	Met	Thr	Ser	Pro	Thr	Ile	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala				
						100			105			110							
Arg	Gly	Ile	Asn	Asn	Ser	Ala	Leu	Trp	Gly	Pro	Gly	Thr	Leu	Val	Thr				
						115			120			125							
Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro				
						130			135			140							
Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr	Leu	Gly	Cys	Leu	Val				
						145			150			155				160			
Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr	Trp	Asn	Ser	Gly	Thr				
						165			170			175							
Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val	Arg	Gln	Ser	Ser	Gly				
						180			185			,	190						
Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr	Ser	Ser	Ser	Gln	Pro				
						195			200			205							
Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn	Thr	Lys	Val	Asp	Lys				
						210			215			220							
Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr	Cys	Pro	Pro	Pro	Glu				
						225			230			235				240			
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Lys	Pro	Lys	Asp				
						245			250			255							
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp				
						260			265			270							
Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr	Trp	Tyr	Ile	Asn	Asn				
						275			280			285							
Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg	Glu	Gln	Gln	Phe	Asn				
						290			295			300							
Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile	Ala	His	Gln	Asp	Trp				
						305			310			315				320			
Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His	Asn	Lys	Ala	Leu	Pro				
						325			330			335							

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu
 340 345 350
 Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg
 355 360 365
 Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile
 370 375 380
 Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr
 385 390 395 400
 Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Asn Lys
 405 410 415
 Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys
 420 425 430
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile
 435 440 445
 Ser Arg Ser Pro Gly Lys
 450

<210> 14
 <211> 1362
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 20D04 anti-CD83 heavy chain sequence

<400> 14
 atggagacag gcctgcgctg gcttctccctg gtcgctgtgc tcaaagggtgt ccagtgtcag 60
 tcgggtggagg agtccccgggg tcgcctggc acgcctggga caccctgtac actcacctgc 120
 accgtctctg gattctccct cagaataacaat gcaataaaact gggtccggca ggctccaggg 180
 aaggggctag agtggatcgg atacatttg ggtgtggc ttacatacta cgcaactgg 240
 gccggaggcc gattcaccat ctccaaaacc tcgactacgg tggatctgaa gatgaccagt 300
 ccgacaaatcg aggacacggc cacctatttc tgtgccagag ggattaataa ctccgctttg 360
 tggggcccaag gcaccctggt caccgtctcc tcagggcaac ctaaggctcc atcagtcttc 420
 ccactggccc cctgctgcgg ggacacacccc tctagcacgg tgaccttggg ctgcctggc 480
 aaaggctacc tcccgagcc agtggactt accttggact cgggcaccc cacaatggg 540
 gtacgcacct tcccgccgt cccgcagttcc tcagccctct actcgctgag cagctggg 600
 agcgtgaccc caagcagcca gcccgtcacc tgcaacgtgg cccacccgc cacaacaccc 660
 aaagtggaca agaccgttgc gccctcgaca tgcagcaagc ccacgtgccc accccctgaa 720
 cttctggggg gaccgtctgt cttcatcttccccaaaaac ccaaggacac cctcatgatc 780
 tcacgcaccc ccgaggtcac atgcgtggg gtggacgtga gccaggatga ccccgagggtg 840
 cagttcacat ggtacataaa caacgagcag gtgcgcaccc cccggccgc gctacgggag 900
 cagcagttca acagcacgat cccgcgtggc agcaccctcc ccatcgccca ccaggactgg 960
 ctgaggggca aggagttcaa gtgcaaaatc cacaacaagg cactccggc ccccatcgag 1020
 aaaaccatct ccaaagccag agggcagccc ctggagccga aggtctacac catggggccct 1080
 ccccgaggag agctgagcag caggtcggtc agcctgaccc gcatgatcaa cggcttctac 1140
 cttccgaca tctcggtgg gtgggagaag aacggaaagg cagaggacaa ctacaagacc 1200
 acggccggcc tgctggacag cgacggcttc tacttctt acaacaagct ctcagtggcc 1260
 acgagttagt ggcagcgggg cgacgtcttc acctgctccg tgatgcacga ggccttgcac 1320
 aaccactaca cgcagaagtc catctccgc tctcgggta aa 1362

<210> 15
 <211> 238
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic 11G05 light chain sequence

<400> 15
 Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
 1 5 10 15

Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala
 20 25 30
 Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser
 35 40 45
 Ser Lys Asn Val Tyr Asn Asn Trp Leu Ser Trp Phe Gln Gln Lys
 50 55 60
 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala
 65 70 75 80
 Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95
 Thr Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr
 100 105 110
 Cys Ala Gly Asp Tyr Ser Ser Ser Asp Asn Gly Phe Gly Gly Gly
 115 120 125
 Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu
 130 135 140
 Phe Pro Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val
 145 150 155 160
 Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val
 165 170 175
 Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln
 180 185 190
 Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr
 195 200 205
 Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln
 210 215 220
 Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
 225 230 235

<210> 16
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 11G05 anti-CD83 light chain sequence

<400> 16

atggacaccca	gggcccccac	tcaagtgcgtg	gggctcctgc	tgctctggct	cccgagggcc	60
agatgtgccg	acgtcgtgat	gaccgacact	ccagccctccg	tgtctgcagc	tgtgggaggc	120
acagtcacca	tcaattgcca	gtccagtaag	aatgtttata	ataacaactg	gttacccctgg	180
tttcagcaga	aaccaggggca	gcctcccaag	ctcctgatct	attatgcatac	cactctggca	240
tctggggtcc	catcgcgggt	cagaggcagtg	ggatctggga	cacagttcac	tctcaccatt	300
agcgacgtgc	agtgtgacga	tgctgcccact	tactactgtg	caggcgattta	tagtagtagt	360
agtgataatg	gtttcggcgg	agggaccgag	gtgggtgtca	aaggtgatcc	agttgcacct	420
actgtcctcc	tcttcccacc	atctagcgat	gagggtggcaa	ctggaacagt	caccatcg	480
tgtgtggcga	ataaaatactt	tcccgtatgtc	accgtcacct	gggaggtggaa	tggcaccacc	540
caaacaactg	gcatcgagaa	cagtaaaaaca	ccgcagaatt	ctgcagattg	tacctacaac	600
ctcagcagca	ctctgacact	gaccagcaca	cagtacaaca	gccacaaaga	gtacacctgc	660
aaggtgaccc	agggcacgac	ctcagtcgtc	cagagctca	gtaggaagaa	ctgttaa	717

<210> 17
 <211> 452
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic 11G05 heavy chain sequence

<400> 17

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5				10					15		

Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
 20 25 30
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Thr Ile Ser
 35 40 45
 Asp Tyr Asp Leu Ser Trp Val Arg Gln Ala Pro Gly Glu Gly Leu Lys
 50 55 60
 Tyr Ile Gly Phe Ile Ala Ile Asp Gly Asn Pro Tyr Tyr Ala Thr Trp
 65 70 75 80
 Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
 85 90 95
 Lys Ile Thr Ala Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
 100 105 110
 Arg Gly Ala Gly Asp Leu Trp Gly Pro Gly Thr Leu Val Thr Val Ser
 115 120 125
 Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro Cys Cys
 130 135 140
 Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val Lys Gly
 145 150 155 160
 Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr Leu Thr
 165 170 175
 Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly Leu Tyr
 180 185 190
 Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro Val Thr
 195 200 205
 Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys Thr Val
 210 215 220
 Ala Pro Ser Thr Cys Ser Lys Pro Thr Cys Pro Pro Pro Glu Leu Leu
 225 230 235 240
 Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp Thr Leu
 245 250 255
 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 260 265 270
 Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn Glu Gln
 275 280 285
 Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn Ser Thr
 290 295 300
 Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp Leu Arg
 305 310 315 320
 Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro Ala Pro
 325 330 335
 Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu Pro Lys
 340 345 350
 Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg Ser Val
 355 360 365
 Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile Ser Val
 370 375 380
 Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr Thr Pro
 385 390 395 400
 Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Asn Lys Leu Ser
 405 410 415
 Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys Ser Val
 420 425 430
 Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile Ser Arg
 435 440 445
 Ser Pro Gly Lys
 450

<210> 18
 <211> 1356
 <212> DNA
 <213> Artificial Sequence

<220>

<223> A synthetic 11G05 anti-CD83 heavy chain sequence

<400> 18

atggagacag	gcctgcgctg	gcttctcctg	gtcgctgtgc	tcaaagggtgt	ccagtgtcag	60
tcggggagg	agtccgggg	tcgcctggc	acgcctggg	caccctgac	actcacctgc	120
acagtctctg	gattcaccat	cagtgactac	gacttgagct	gggtccggca	ggctccaggg	180
gaggggctga	aatacatcg	attcattgt	attgatggta	accatacta	cgcacctgg	240
gaaaaaggcc	gattcaccat	ctccaaaacc	tcgaccacgg	tggatctgaa	aatcaccgct	300
ccgacaaccg	aagacacggc	cacgtatttc	tgtgccagag	gggcagggga	cctctggggc	360
ccagggacc	tcgtcaccgt	ctcttcaggg	caacctaagg	ctccatcagt	cttcccactg	420
gccccctgct	gcggggacac	accctctagc	acggtgacct	tgggctgcct	ggtcaaaggc	480
tacctcccgg	agccagtgc	cgtgacctgg	aactcgggca	ccctcacc	tgggtacgc	540
acctcccg	ccgtccggca	gtcctcaggc	ctctactcgc	tgagcagcgt	gttgagcgtg	600
acctcaagca	gccagccgt	cacctgcaac	gtggcccacc	cagccaccaa	caccaaagtg	660
gacaagac	ttgcgccctc	gacatgcagc	aagcccacgt	gcccacccccc	tgaactcctg	720
gggggaccgt	ctgtcttcat	cttcccccca	aaacccaagg	acaccctcat	gatctcacgc	780
accccccgg	tcacatgcgt	ggtggtgac	gtgagccagg	atgaccccg	gtgtcagttc	840
acatggtaca	taaacaaacga	gcaggtgcgc	accggccggc	cgccgtacg	ggagcagcag	900
ttcaacagca	cgatccgcgt	ggtcagcacc	ctccccatcg	cgcaccagga	ctggctgagg	960
gcaaggagt	tcaagtgc	aa	gtccacaac	aaggcactcc	cgccccccat	1020
atctccaaag	ccagagggca	gcccctggag	ccgaaggct	acaccatggg	ccctccccgg	1080
gaggagctga	gcagcagg	ggtcagc	acctgc	tcaacgg	ctacccttcc	1140
gacatctcg	ttggagtgg	gaagaacggg	aaggcagg	acaactaca	gaccacgg	1200
gccgtctgg	acagcgacgg	ctcctacttc	ctctacaaca	agctctc	gcccacg	1260
gagtggc	ggggcgacgt	cttcac	ctcg	tgatgc	acgaggc	1320
tacacgcaga	agtccatctc	ccgctctccg	ggtaaa			1356

<210> 19

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<221> SITE

<222> (1) . . . (238)

<223> Xaa = any amino acid

<220>

<223> A synthetic 14C12 light chain sequence

<400> 19

Met	Asp	Xaa	Arg	Ala	Pro	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Trp		
1				5				10					15			
Leu	Pro	Gly	Ala	Arg	Cys	Ala	Leu	Val	Met	Thr	Gln	Thr	Pro	Ala	Ser	
							20		25				30			
Val	Ser	Ala	Ala	Ala	Val	Gly	Gly	Thr	Val	Thr	Ile	Asn	Cys	Gln	Ser	Ser
							35		40			45				
Gln	Ser	Val	Tyr	Asp	Asn	Asp	Glu	Leu	Ser	Trp	Tyr	Gln	Gln	Lys	Pro	
							50		55			60				
Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Leu	Ala	Ser	Lys	Leu	Ala	Ser	
							65		70		75		80			
Gly	Val	Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Ala	
							85		90			95				
Leu	Thr	Ile	Ser	Gly	Val	Gln	Cys	Asp	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	
							100		105			110				
Gln	Ala	Thr	His	Tyr	Ser	Ser	Asp	Trp	Tyr	Leu	Thr	Phe	Gly	Gly	Gly	
							115		120			125				
Thr	Glu	Val	Val	Val	Lys	Gly	Asp	Pro	Val	Ala	Pro	Thr	Val	Leu	Leu	
							130		135			140				
Phe	Pro	Pro	Ser	Ser	Asp	Glu	Val	Ala	Thr	Gly	Thr	Val	Thr	Ile	Val	
							145		150			155		160		

Cys Val Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val
 165 170 175
 Asp Gly Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln
 180 185 190
 Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr
 195 200 205
 Ser Thr Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln
 210 215 220
 Gly Thr Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
 225 230 235

<210> 20
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 14C12 anti-CD83 light chain sequence

<400> 20
 atggacattra gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60
 agatgtgccctt tttgtatgac ccagactcca gcctccgtgt ctgcagctgt gggaggcaca 120
 gtcaccatca attgcacgtc cagtcagagt gtttatgata acgacgaatt atcctggtat 180
 cagcagaaac caggcagcc tcccaagctc ctgatctatc tggcatccaa gttggcatct 240
 ggggtccccat cccgattcaa aggcaagtga tctggacac agttcgctct caccatcagc 300
 ggcgtgcagt gtgacgatgc tgccacttac tactgtcaag ccactcatta tagtagtgat 360
 tggtatctta ctttcggcgg agggaccgag gtgggtgtca aagggtatcc agttgcacct 420
 actgtcctcc tcttcccacc atctagcgtat gaggtggcaa ctggaacagt caccatcgtg 480
 tggatggcgataaaaatctt tcccgatgtc accgtcacct gggaggtgga tggcaccacc 540
 caaacaaactg gcatcgagaa cagtaaaaca ccgcagaatt ctgcagattt tacctacaac 600
 ctcagcagca ctctgacact gaccagcaca cagtacaaca gccacaaaaga gtacacctgc 660
 aaggtgaccc agggcacgac ctcagtcgtc cagagcttca gtaggaagaa ctgttaa 717

<210> 21
 <211> 454
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic 14C12 heavy chain sequence

<400> 21
 Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
 1 5 10 15
 Val His Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
 20 25 30
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Arg Ser
 35 40 45
 Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 50 55 60
 Trp Val Gly Val Ile Ser Thr Ala Tyr Asn Ser His Tyr Ala Ser Trp
 65 70 75 80
 Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu
 85 90 95
 Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
 100 105 110
 Arg Gly Gly Ser Trp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr
 115 120 125
 Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro
 130 135 140
 Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys Leu Val
 145 150 155 160

Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Thr
 165 170 175
 Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser Ser Gly
 180 185 190
 Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser Gln Pro
 195 200 205
 Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val Asp Lys
 210 215 220
 Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Thr Cys Pro Pro Pro Glu
 225 230 235 240
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro Lys Asp
 245 250 255
 Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
 260 265 270
 Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile Asn Asn
 275 280 285
 Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln Phe Asn
 290 295 300
 Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln Asp Trp
 305 310 315 320
 Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala Leu Pro
 325 330 335
 Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro Leu Glu
 340 345 350
 Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser Ser Arg
 355 360 365
 Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser Asp Ile
 370 375 380
 Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr Lys Thr
 385 390 395 400
 Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr Asn Lys
 405 410 415
 Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe Thr Cys
 420 425 430
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Ile
 435 440 445
 Ser Arg Ser Pro Gly Lys
 450

<210> 22
 <211> 1362
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic 14C12 anti-CD83 heavy chain sequence

<400> 22

Ala	Thr	Gly	Gly	Ala	Gly	Ala	Cys	Ala	Gly	Gly	Cys	Cys	Thr	Gly	Cys
1				5				10					15		
Gly	Cys	Thr	Gly	Gly	Cys	Thr	Thr	Cys	Thr	Cys	Cys	Thr	Gly	Gly	Thr
					20			25					30		
Cys	Gly	Cys	Thr	Gly	Thr	Gly	Cys	Thr	Cys	Ala	Ala	Ala	Gly	Gly	Thr
					35			40					45		
Gly	Thr	Cys	Cys	Ala	Cys	Thr	Gly	Thr	Cys	Ala	Gly	Thr	Cys	Gly	Gly
					50			55					60		
Thr	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Thr	Cys	Gly	Gly	Gly	Gly	Gly	Gly
						65			70				75		80
Thr	Cys	Gly	Cys	Cys	Thr	Gly	Gly	Thr	Cys	Ala	Cys	Gly	Cys	Cys	Thr
						85			90				95		
Gly	Gly	Gly	Ala	Cys	Ala	Cys	Cys	Cys	Thr	Gly	Ala	Cys	Ala	Cys	
					100			105					110		

Thr Cys Ala Cys Cys Thr Gly Cys Ala Cys Ala Gly Cys Cys Thr Cys
 115 120 125
 Thr Gly Gly Ala Thr Thr Cys Thr Cys Cys Gly Cys Ala Gly Cys
 130 135 140
 Ala Gly Cys Thr Ala Cys Gly Ala Cys Ala Thr Gly Ala Gly Cys Thr
 145 150 155 160
 Gly Gly Gly Thr Cys Cys Gly Cys Cys Ala Gly Gly Cys Thr Cys Cys
 165 170 175
 Ala Gly Gly Ala Ala Gly Gly Cys Thr Gly Gly Ala Ala
 180 185 190
 Thr Gly Gly Gly Thr Cys Gly Gly Ala Gly Thr Cys Ala Thr Thr Ala
 195 200 205
 Gly Thr Ala Cys Thr Gly Cys Thr Thr Ala Thr Ala Ala Cys Thr Cys
 210 215 220
 Ala Cys Ala Cys Thr Ala Cys Gly Cys Gly Ala Gly Cys Thr Gly Gly
 225 230 235 240
 Gly Cys Ala Ala Ala Gly Gly Cys Cys Gly Ala Thr Thr Cys Ala
 245 250 255
 Cys Cys Ala Thr Cys Thr Cys Ala Gly Ala Ala Cys Cys Thr Cys
 260 265 270
 Gly Ala Cys Cys Ala Cys Gly Gly Thr Gly Gly Ala Thr Cys Thr Gly
 275 280 285
 Ala Ala Ala Ala Thr Gly Ala Cys Cys Ala Gly Thr Cys Thr Gly Ala
 290 295 300
 Cys Ala Ala Cys Cys Gly Ala Ala Gly Ala Cys Ala Cys Gly Gly Cys
 305 310 315 320
 Cys Ala Cys Cys Thr Ala Thr Thr Cys Thr Gly Thr Gly Cys Cys
 325 330 335
 Ala Gly Ala Gly Gly Gly Thr Ala Gly Thr Thr Gly Gly Thr
 340 345 350
 Thr Gly Gly Ala Thr Cys Thr Cys Thr Gly Gly Gly Cys Cys Ala
 355 360 365
 Gly Gly Gly Cys Ala Cys Cys Cys Thr Gly Gly Thr Cys Ala Cys Cys
 370 375 380
 Gly Thr Cys Thr Cys Cys Thr Cys Ala Gly Gly Cys Ala Ala Cys
 385 390 395 400
 Cys Thr Ala Ala Gly Gly Cys Thr Cys Cys Ala Thr Cys Ala Gly Thr
 405 410 415
 Cys Thr Thr Cys Cys Ala Cys Thr Gly Gly Cys Cys Cys Cys Cys
 420 425 430
 Thr Gly Cys Thr Gly Cys Gly Gly Ala Cys Ala Cys Ala Cys
 435 440 445
 Cys Cys Thr Cys Thr Ala Gly Cys Ala Cys Gly Gly Thr Gly Ala Cys
 450 455 460
 Cys Thr Thr Gly Gly Cys Thr Gly Cys Cys Thr Gly Gly Thr Cys
 465 470 475 480
 Ala Ala Ala Gly Gly Cys Thr Ala Cys Cys Thr Cys Cys Cys Gly Gly
 485 490 495
 Ala Gly Cys Cys Ala Gly Thr Gly Ala Cys Cys Gly Thr Gly Ala Cys
 500 505 510
 Cys Thr Gly Gly Ala Ala Cys Thr Cys Gly Gly Cys Ala Cys Cys
 515 520 525
 Cys Thr Cys Ala Cys Cys Ala Ala Thr Gly Gly Gly Thr Ala Cys
 530 535 540
 Gly Cys Ala Cys Cys Thr Thr Cys Cys Gly Thr Cys Cys Gly Thr
 545 550 555 560
 Cys Cys Gly Gly Cys Ala Gly Thr Cys Cys Thr Cys Ala Gly Gly Cys
 565 570 575
 Cys Thr Cys Thr Ala Cys Thr Cys Gly Cys Thr Gly Ala Gly Cys Ala
 580 585 590
 Gly Cys Gly Thr Gly Gly Thr Gly Ala Gly Cys Gly Thr Gly Ala Cys
 595 600 605

Cys Thr Cys Ala Ala Gly Cys Ala Gly Cys Cys Ala Gly Cys Cys Cys
 610 615 620
 Gly Thr Cys Ala Cys Cys Thr Gly Cys Ala Ala Cys Gly Thr Gly Gly
 625 630 635 640
 Cys Cys Cys Ala Cys Cys Ala Gly Cys Cys Ala Cys Cys Ala Ala
 645 650 655
 Cys Ala Cys Cys Ala Ala Ala Gly Thr Gly Gly Ala Cys Ala Ala Gly
 660 665 670
 Ala Cys Cys Gly Thr Thr Gly Cys Gly Cys Cys Thr Cys Gly Ala
 675 680 685
 Cys Ala Thr Gly Cys Ala Gly Cys Ala Ala Gly Cys Cys Cys Ala Cys
 690 695 700
 Gly Thr Gly Cys Cys Cys Ala Cys Cys Cys Cys Thr Gly Ala Ala
 705 710 715 720
 Cys Thr Cys Cys Thr Gly Gly Gly Gly Ala Cys Cys Gly Thr
 725 730 735
 Cys Thr Gly Thr Cys Thr Cys Ala Thr Cys Thr Thr Cys Cys Cys
 740 745 750
 Cys Cys Cys Ala Ala Ala Ala Cys Cys Cys Ala Ala Gly Gly Ala Cys
 755 760 765
 Ala Cys Cys Cys Thr Cys Ala Thr Gly Ala Thr Cys Thr Cys Ala Cys
 770 775 780
 Gly Cys Ala Cys Cys Cys Cys Gly Ala Gly Gly Thr Cys Ala Cys
 785 790 795 800
 Ala Thr Gly Cys Gly Thr Gly Gly Thr Gly Thr Gly Ala Cys
 805 810 815
 Gly Thr Gly Ala Gly Cys Cys Ala Gly Gly Ala Thr Gly Ala Cys Cys
 820 825 830
 Cys Cys Gly Ala Gly Gly Thr Gly Cys Ala Gly Thr Thr Cys Ala Cys
 835 840 845
 Ala Thr Gly Gly Thr Ala Cys Ala Thr Ala Ala Ala Cys Ala Ala Cys
 850 855 860
 Gly Ala Gly Cys Ala Gly Gly Thr Gly Cys Gly Cys Ala Cys Cys Gly
 865 870 875 880
 Cys Cys Cys Gly Gly Cys Cys Gly Cys Cys Thr Ala Cys Gly
 885 890 895
 Gly Gly Ala Gly Cys Ala Gly Cys Ala Gly Thr Thr Cys Ala Ala Cys
 900 905 910
 Ala Gly Cys Ala Cys Gly Ala Thr Cys Cys Gly Cys Gly Thr Gly Gly
 915 920 925
 Thr Cys Ala Gly Cys Ala Cys Cys Cys Thr Cys Cys Cys Ala Thr
 930 935 940
 Cys Gly Cys Gly Cys Ala Cys Cys Ala Gly Gly Ala Cys Thr Gly Gly
 945 950 955 960
 Cys Thr Gly Ala Gly Gly Gly Cys Ala Ala Gly Gly Ala Gly Thr
 965 970 975
 Thr Cys Ala Ala Gly Thr Gly Cys Ala Ala Ala Gly Thr Cys Cys Ala
 980 985 990
 Cys Ala Ala Cys Ala Ala Gly Gly Cys Ala Cys Thr Cys Cys Cys Gly
 995 1000 1005
 Gly Cys Cys Cys Cys Ala Thr Cys Gly Ala Gly Ala Ala Ala Ala
 1010 1015 1020
 Cys Cys Ala Thr Cys Thr Cys Cys Ala Ala Ala Gly Cys Cys Ala Gly
 1025 1030 1035 1040
 Ala Gly Gly Cys Ala Gly Cys Cys Cys Cys Thr Gly Gly Ala Gly
 1045 1050 1055
 Cys Cys Gly Ala Ala Gly Gly Thr Cys Thr Ala Cys Ala Cys Cys Ala
 1060 1065 1070
 Thr Gly Gly Cys Cys Cys Thr Cys Cys Cys Cys Gly Gly Gly Ala
 1075 1080 1085
 Gly Gly Ala Gly Cys Thr Gly Ala Gly Cys Ala Gly Cys Ala Gly Gly
 1090 1095 1100

Thr Cys Gly Gly Thr Cys Ala Gly Cys Cys Thr Gly Ala Cys Cys Thr
 1105 1110 1115 1120
 Gly Cys Ala Thr Gly Ala Thr Cys Ala Ala Cys Gly Gly Cys Thr Thr
 1125 1130 1135
 Cys Thr Ala Cys Cys Cys Thr Thr Cys Cys Gly Ala Cys Ala Thr Cys
 1140 1145 1150
 Thr Cys Gly Gly Thr Gly Gly Ala Gly Thr Gly Gly Ala Gly Ala
 1155 1160 1165
 Ala Gly Ala Ala Cys Gly Gly Ala Ala Gly Gly Cys Ala Gly Ala
 1170 1175 1180
 Gly Gly Ala Cys Ala Ala Cys Thr Ala Cys Ala Ala Gly Ala Cys Cys
 1185 1190 1195 1200
 Ala Cys Gly Cys Cys Gly Gly Cys Cys Gly Thr Gly Cys Thr Gly Gly
 1205 1210 1215
 Ala Cys Ala Gly Cys Gly Ala Cys Gly Gly Cys Thr Cys Cys Thr Ala
 1220 1225 1230
 Cys Thr Thr Cys Cys Thr Cys Thr Ala Cys Ala Ala Cys Ala Ala Gly
 1235 1240 1245
 Cys Thr Cys Thr Cys Ala Gly Thr Gly Cys Cys Cys Ala Cys Gly Ala
 1250 1255 1260
 Gly Thr Gly Ala Gly Thr Gly Gly Cys Ala Gly Cys Gly Gly Gly
 1265 1270 1275 1280
 Cys Gly Ala Cys Gly Thr Cys Thr Thr Cys Ala Cys Cys Thr Gly Cys
 1285 1290 1295
 Thr Cys Cys Gly Thr Gly Ala Thr Gly Cys Ala Cys Gly Ala Gly Gly
 1300 1305 1310
 Cys Cys Thr Thr Gly Cys Ala Cys Ala Ala Cys Cys Ala Cys Thr Ala
 1315 1320 1325
 Cys Ala Cys Gly Cys Ala Gly Ala Ala Gly Thr Cys Cys Ala Thr Cys
 1330 1335 1340
 Thr Cys Cys Cys Gly Cys Thr Cys Thr Cys Cys Gly Gly Gly Thr Ala
 1345 1350 1355 1360
 Ala Ala

<210> 23
 <211> 5
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 23
 Ser Tyr Asp Met Thr
 1 5

<210> 24
 <211> 5
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 24
 Ser Tyr Asp Met Ser
 1 5

<210> 25
 <211> 5
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 25
 Asp Tyr Asp Leu Ser
 1 5

<210> 26
<211> 5
<212> PRT
<213> Oryctolagus cuniculus

<400> 26
Ser Tyr Asp Met Ser
1 5

<210> 27
<211> 8
<212> PRT
<213> Oryctolagus cuniculus

<400> 27
Tyr Ala Ser Gly Ser Thr Tyr Tyr
1 5

<210> 28
<211> 8
<212> PRT
<213> Oryctolagus cuniculus

<400> 28
Ser Ser Ser Gly Thr Thr Tyr Tyr
1 5

<210> 29
<211> 8
<212> PRT
<213> Oryctolagus cuniculus

<400> 29
Tyr Ala Ser Gly Ser Thr Tyr Tyr
1 5

<210> 30
<211> 8
<212> PRT
<213> Oryctolagus cuniculus

<400> 30
Ala Ile Asp Gly Asn Pro Tyr Tyr
1 5

<210> 31
<211> 8
<212> PRT
<213> Oryctolagus cuniculus

<400> 31
Ser Thr Ala Tyr Asn Ser His Tyr
1 5

<210> 32
<211> 11
<212> PRT
<213> Oryctolagus cuniculus

<400> 32
Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His
1 5 10

<210> 33
<211> 8
<212> PRT
<213> Oryctolagus cuniculus

<400> 33
Glu Gly Ala Gly Val Ser Met Thr
1 5

<210> 34
<211> 8
<212> PRT
<213> Oryctolagus cuniculus

<400> 34
Glu Asp Ala Gly Phe Ser Asn Ala
1 5

<210> 35
<211> 4
<212> PRT
<213> Oryctolagus cuniculus

<400> 35
Gly Ala Gly Asp
1

<210> 36
<211> 6
<212> PRT
<213> Oryctolagus cuniculus

<400> 36
Gly Gly Ser Trp Leu Asp
1 5

<210> 37
<211> 5
<212> PRT
<213> Oryctolagus cuniculus

<400> 37
Arg Cys Ala Tyr Asp
1 5

<210> 38
<211> 6
<212> PRT
<213> Oryctolagus cuniculus

<400> 38
Arg Cys Ala Asp Val Val
1 5

<210> 39
<211> 5
<212> PRT
<213> Oryctolagus cuniculus

<400> 39
Arg Cys Ala Leu Val
1 5

<210> 40
<211> 6
<212> PRT
<213> Oryctolagus cuniculus

<400> 40
Gln Ser Ile Ser Thr Tyr
1 5

<210> 41
<211> 6
<212> PRT
<213> Oryctolagus cuniculus

<400> 41
Gln Ser Val Ser Ser Tyr
1 5

<210> 42
<211> 6
<212> PRT
<213> Oryctolagus cuniculus

<400> 42
Glu Ser Ile Ser Asn Tyr
1 5

<210> 43
<211> 8
<212> PRT
<213> Oryctolagus cuniculus

<400> 43
Lys Asn Val Tyr Asn Asn Asn Trp
1 5

<210> 44
<211> 12
<212> PRT
<213> Oryctolagus cuniculus

<400> 44
Gln Gln Gly Tyr Thr His Ser Asn Val Asp Asn Val
1 5 10

<210> 45
<211> 12
<212> PRT
<213> Oryctolagus cuniculus

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<400> 45
Gln Gln Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala
 1           5           10

<210> 46
<211> 14
<212> PRT
<213> Oryctolagus cuniculus

<400> 46
Gln Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala
 1           5           10

<210> 47
<211> 11
<212> PRT
<213> Oryctolagus cuniculus

<400> 47
Ala Gly Asp Tyr Ser Ser Ser Asp Asn Gly
 1           5           10

<210> 48
<211> 12
<212> PRT
<213> Oryctolagus cuniculus

<400> 48
Gln Ala Thr His Tyr Ser Ser Asp Trp Leu Thr Tyr
 1           5           10

<210> 49
<211> 5
<212> RNA
<213> Oryctolagus cuniculus

<400> 49
auuuua                                5

<210> 50
<211> 6
<212> RNA
<213> Oryctolagus cuniculus          ↴

<400> 50
auuuuua                                6

<210> 51
<211> 7
<212> RNA
<213> Oryctolagus cuniculus

<400> 51
auuuuuua                                7

<210> 52
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 heavy chain variable region sequence

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<400> 52
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20 25 30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser
35 40 45
Ser Tyr Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60
Trp Ile Gly Ile Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp
65 70 75 80
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
85 90 95
Glu Val Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ser
100 105 110
Arg Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His Leu Trp Gly Pro
115 120 125
Gly Thr Leu Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val
130 135 140
Phe Pro Leu Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser
145 150 155

<210> 53
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 heavy chain variable region
sequence

<400> 53
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Ser Pro
20 25 30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser
35 40 45
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60
Tyr Ile Gly Ile Ile Ser Ser Gly Thr Thr Tyr Tyr Ala Asn Trp
65 70 75 80
Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
85 90 95
Lys Val Thr Ser Pro Thr Ile Gly Asp Thr Ala Thr Tyr Phe Cys Ala
100 105 110
Arg Glu Gly Ala Gly Val Ser Met Thr Leu Trp Gly Pro Gly Thr Leu
115 120 125
Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
130 135 140
Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser
145 150

<210> 54
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 heavy chain variable region
sequence

<400> 54
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
1 5 10 15
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
20 25 30
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser
35 40 45
Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60
Trp Ile Gly Ile Ile Tyr Ala Ser Gly Ser Thr Tyr Tyr Ala Ser Trp
65 70 75 80
Ala Lys Gly Arg Val Ala Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
85 90 95
Lys Ile Thr Ser Pro Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
100 105 110
Arg Glu Asp Ala Gly Phe Ser Asn Ala Leu Trp Gly Pro Gly Thr Leu
115 120 125
Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
130 135 140
Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser
145 150

<210> 55

<211> 147

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 light chain variable region sequence

<400> 55

Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser
20 25 30
Val Glu Val Ala Val Gly Gly Thr Val Thr Ile Lys Cys Gln Ala Ser
35 40 45
Gln Ser Ile Ser Thr Tyr Leu Asp Trp Tyr Gln Gln Lys Pro Gly Gln
50 55 60
Pro Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Ala Ser Gly Val
65 70 75 80
Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr Leu Thr
85 90 95
Ile Ser Asp Leu Glu Cys Ala Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Gly Tyr Thr His Ser Asn Val Asp Asn Val Phe Gly Gly Thr Glu
115 120 125
Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro
130 135 140
Pro Ser Ser
145

<210> 56

<211> 147

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic anti-CD83 light chain variable region sequence

<400> 56
Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser
20 25 30
Val Glu Val Ala Val Gly Gly Thr Val Ala Ile Lys Cys Gln Ala Ser
35 40 45
Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
50 55 60
Pro Pro Lys Pro Leu Ile Tyr Glu Ala Ser Met Leu Ala Ala Gly Val
65 70 75 80
Ser Ser Arg Phe Lys Gly Ser Gly Thr Asp Phe Thr Leu Thr
85 90 95
Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100 105 110
Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala Phe Gly Gly Thr Glu
115 120 125

Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro
130 135 140
Pro Ser Ser
145

<210> 57
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 light chain variable region sequence

<400> 57
Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala
20 25 30
Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ala
35 40 45
Ser Glu Ser Ile Ser Asn Tyr Leu Ser Trp Tyr Gln Gln Lys Pro Gly
50 55 60
Gln Pro Pro Lys Leu Leu Ile Tyr Arg Thr Ser Thr Leu Ala Ser Gly
65 70 75 80
Val Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Glu Tyr Thr Leu
85 90 95
Thr Ile Ser Gly Val Gln Cys Asp Asp Val Ala Thr Tyr Tyr Cys Gln
100 105 110
Cys Thr Ser Gly Gly Lys Phe Ile Ser Asp Gly Ala Ala Phe Gly Gly
115 120 125
Gly Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu
130 135 140
Leu Phe Pro Pro Ser Ser
145 150

<210> 58
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic M83 020B08L light chain sequence

<400> 58

Met	Asp	Met	Arg	Ala	Pro	Thr	Gln	Leu	Leu	Gly	Leu	Leu	Leu	Trp		
1								5			10			15		
Leu	Pro	Gly	Ala	Arg	Cys	Ala	Tyr	Asp	Met	Thr	Gln	Thr	Pro	Ala	Ser	
									20		25			30		
Val	Glu	Val	Ala	Val	Gly	Gly	Thr	Val	Thr	Ile	Lys	Cys	Gln	Ala	Ser	
									35		40			45		
Gln	Ser	Ile	Ser	Thr	Tyr	Leu	Asp	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
									50		55			60		
Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Asp	Ala	Ser	Asp	Leu	Ala	Ser	Gly	Val	
									65		70			75		80
Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe	Thr	Leu	Thr	
									85		90			95		
Ile	Ser	Asp	Leu	Glu	Cys	Ala	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	
									100		105			110		
Gly	Tyr	Thr	His	Ser	Asn	Val	Asp	Asn	Val	Phe	Gly	Gly	Thr	Glu		
									115		120			125		
Val	Val	Val	Lys	Gly	Asp	Pro	Val	Ala	Pro	Thr	Val	Leu	Leu	Phe	Pro	
									130		135			140		
Pro	Ser	Ser	Asp	Glu	Val	Ala	Thr	Gly	Thr	Val	Thr	Ile	Val	Cys	Val	
									145		150			155		160
Ala	Asn	Lys	Tyr	Phe	Pro	Asp	Val	Thr	Val	Thr	Trp	Glu	Val	Asp	Gly	
									165		170			175		
Thr	Thr	Gln	Thr	Thr	Gly	Ile	Glu	Asn	Ser	Lys	Thr	Pro	Gln	Asn	Ser	
									180		185			190		
Ala	Asp	Cys	Thr	Tyr	Asn	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Thr	Ser	Thr	
									195		200			205		
Gln	Tyr	Asn	Ser	His	Lys	Glu	Tyr	Thr	Cys	Lys	Val	Thr	Gln	Gly	Thr	
									210		215			220		
Thr	Ser	Val	Val	Gln	Ser	Phe	Ser	Arg	Lys	Asn	Cys					
									225		230			235		

<210> 59

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic M83 020B08L anti-CD83 light chain sequence

<400> 59

atggacatga	gggcccccac	tcaagtgcgt	gggctcctgc	tgctctggct	cccgagggcc	60
agatgtgcct	atgatatgac	ccagactcca	gcctctgtgg	aggttagctgt	gggaggcaca	120
gtcaccatca	agtgcaggc	cagtcagagc	attagtagctt	acttagactg	gtatcagcag	180
aaaccagggc	agcctcccaa	gctcctgtat	tatgtatgtat	ccgatctggc	atctggggtc	240
ccatcgcggt	tcaaaaggcag	tggatctggg	acacagttca	ctctcaccat	cagcgacctg	300
gagtgtgcgg	atgctccac	ttactactgt	caacagggtt	atacacatag	taatgttgat	360
aatgttttcg	gcccggggac	cgagggtggg	gtcaaagggt	atccagggtc	acctactgtc	420
ctccctttcc	caccatctag	cgatgagggt	gcaactggaa	cagtcaccat	cgtgtgtgt	480
gcaataaaat	actttcccgaa	tgtcaccgtc	acctggggagg	tggatggcac	cacccaaaca	540
actggcatcg	agaacagtaa	aacaccgcag	aattctgcag	attgtaccta	caacctcagc	600
agcaactctga	cactgaccag	cacacagtac	aacagccaca	aagagtacac	ctgcaagggtg	660
acccaggggca	cgacccatcg	cgtccagagc	ttcagtagga	agaactgtta	a	711

<210> 60

<211> 456

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic M83 020B08H heavy chain sequence

<400> 60
 Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly
 1 5 10 15
 Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro
 20 25 30
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Phe Ser Leu Ser
 35 40 45
 Ser Tyr Asp Met Thr Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 50 55 60
 Trp Ile Gly Ile Ile Tyr Ala Ser Gly Thr Thr Tyr Tyr Ala Asn Trp
 65 70 75 80
 Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
 85 90 95
 Lys Val Thr Ser Pro Thr Ile Gly Asp Thr Ala Thr Tyr Phe Cys Ala
 100 105 110
 Arg Glu Gly Ala Gly Val Ser Met Thr Leu Trp Gly Pro Gly Thr Leu
 115 120 125
 Val Thr Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu
 130 135 140
 Ala Pro Cys Cys Gly Asp Thr Pro Ser Ser Thr Val Thr Leu Gly Cys
 145 150 155 160
 Leu Val Lys Gly Tyr Leu Pro Glu Pro Val Thr Val Thr Trp Asn Ser
 165 170 175
 Gly Thr Leu Thr Asn Gly Val Arg Thr Phe Pro Ser Val Arg Gln Ser
 180 185 190
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Ser Val Thr Ser Ser Ser
 195 200 205
 Gln Pro Val Thr Cys Asn Val Ala His Pro Ala Thr Asn Thr Lys Val
 210 215 220
 Asp Lys Thr Val Ala Pro Ser Thr Cys Ser Lys Pro Thr Cys Pro Pro
 225 230 235 240
 Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Pro
 245 250 255
 Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
 260 265 270
 Val Asp Val Ser Gln Asp Asp Pro Glu Val Gln Phe Thr Trp Tyr Ile
 275 280 285
 Asn Asn Glu Gln Val Arg Thr Ala Arg Pro Pro Leu Arg Glu Gln Gln
 290 295 300
 Phe Asn Ser Thr Ile Arg Val Val Ser Thr Leu Pro Ile Ala His Gln
 305 310 315 320
 Asp Trp Leu Arg Gly Lys Glu Phe Lys Cys Lys Val His Asn Lys Ala
 325 330 335
 Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Arg Gly Gln Pro
 340 345 350
 Leu Glu Pro Lys Val Tyr Thr Met Gly Pro Pro Arg Glu Glu Leu Ser
 355 360 365
 Ser Arg Ser Val Ser Leu Thr Cys Met Ile Asn Gly Phe Tyr Pro Ser
 370 375 380
 Asp Ile Ser Val Glu Trp Glu Lys Asn Gly Lys Ala Glu Asp Asn Tyr
 385 390 395 400
 Lys Thr Thr Pro Ala Val Leu Asp Ser Asp Gly Ser Tyr Phe Leu Tyr
 405 410 415
 Asn Lys Leu Ser Val Pro Thr Ser Glu Trp Gln Arg Gly Asp Val Phe
 420 425 430
 Thr Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 435 440 445
 Ser Ile Ser Arg Ser Pro Gly Lys
 450 455

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<210> 61
<211> 1368
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic M83 020B08H anti-CD83 heavy chain
sequence

<400> 61
atggagacag gcctgcgctg gcttctcccg gtcgctgtgc tcaaagggtgt ccagtgtcag 60
tcggtgagg agtccccggg tcgcctggc acgcctggg caccctgtac actcacctgc 120
acagtctctg gattctccct cagcagctac gacatgacct gggcccgcca ggctccagg 180
aaggggctgg aatggatcgg aatcatttat gctagtggta ccacatacta cgcaactgg 240
gcgaaaaggcc gattcaccat ctccaaaaacc tcgaccacgg tggatctgaa agtaccagg 300
ccgacaatcg gggacacggc cacctattc tgtgccagag aaaaaaaaaa tgtagtatg 360
actttgtggg gcccaggcac cctggtcacc gtctcttcgg ggcaacccaa ggctccatca 420
gtcttccac tggcccccctg ctgcggggac acaccctcta gcacgggtac cttggctgc 480
ctggtcaaaag gtcacctccc ggagccaggc accgtgaccc ggaactctggg caccctcacc 540
aatggggtaac gcacccccc gtccgtccgg cagtccttcgg gcctctactc gctgagcagc 600
gtggtgagcg tgacctaag cagccagccc gtcacccatgc acgtggccca cccagccacc 660
aacacccaaag tggacaagac cgttgcgcgc tcgacatgcg gcaagccac gtggccaccc 720
cctgaactcc tggggggacc gtctgtcttc atctccccc caaaaaaaaa ggacaccctc 780
atgatctcac gcacccccc gtcacatgc gtgggtgtgg acgtgagccca ggatgacccc 840
gaggtgcagt tcacatggta cataaaacaac gagcagggtgc gcacccggcc gccggcccta 900
cgggagcagc agttcaacacg cacgatccgc gtggtagca ccctcccat cgcgcaccag 960
gactggctga gggggcaaggaa gttcaaggta aaagtccaca acaaggcact cccggccccc 1020
atcgagaaaaa ccatctccaa agccagaggc cagccctgg agccgaaggc ctacaccatg 1080
ggccctcccc gggaggagct gaggcaggc tcggtagcc tgacccatgc gatcaacggc 1140
ttctaccctt ccgacatctc ggtggagttgg gagaagaacg ggaaggcaga ggacaactac 1200
aagaccacgc cggccgtgt ggacagcgcg ggctctact tcctctacaa caagctctca 1260
gtgcccacga gtgagtgccg gccccggcgcac gtcttcaccc gtcctgtat gcacgaggcc 1320
ttgcacaacc actacacgcgaa gaaatccatc tcccgctctc cgggtaaa 1368

<210> 62
<211> 236
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic M83 006G05L light chain sequence

<400> 62
Met Asp Met Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
 1           5          10          15
Leu Pro Gly Ala Arg Cys Ala Tyr Asp Met Thr Gln Thr Pro Ala Ser
 20          25          30
Val Glu Val Ala Val Gly Gly Thr Val Ala Ile Lys Cys Gln Ala Ser
 35          40          45
Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
 50          55          60
Pro Pro Lys Pro Leu Ile Tyr Glu Ala Ser Met Leu Ala Ala Gly Val
 65          70          75          80
Ser Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
 85          90          95
Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys Gln Gln
100          105         110
Gly Tyr Ser Ile Ser Asp Ile Asp Asn Ala Phe Gly Gly Gly Thr Glu
115          120          125
Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu Phe Pro
130          135          140

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Pro Ser Ser Asp Glu Val Ala Thr Gly Thr Val Thr Ile Val Cys Val
 145 150 155 160
 Ala Asn Lys Tyr Phe Pro Asp Val Thr Val Thr Trp Glu Val Asp Gly
 165 170 175
 Thr Thr Gln Thr Thr Gly Ile Glu Asn Ser Lys Thr Pro Gln Asn Ser
 180 185 190
 Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu Thr Ser Thr
 195 200 205
 Gln Tyr Asn Ser His Lys Glu Tyr Thr Cys Lys Val Thr Gln Gly Thr
 210 215 220
 Thr Ser Val Val Gln Ser Phe Ser Arg Lys Asn Cys
 225 230 235

<210> 63
 <211> 711
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic M83 006G05L anti-CD83 light chain sequence

<400> 63
 atggacatga gggcccccac tcaactgctg gggctcctgc tgctctggct cccaggtgcc 60
 agatgtgcct atgatatgac ccagactcca gcctctgtgg aggttagctgt gggaggcaca 120
 gtcGCCatca agtGCCAGGC cagttagAGC gtttagtagtt acttagcctg gtatcagcag 180
 aaaccaggGC agcCTCCaa gcccctgatc tacGAAGCAT ccATGCTGGC ggCTGGGTC 240
 tcATCGCGGT tcaaAGGCAG tggatCTGGG acAGATTCA ctCTCACCAT cAGCgACCTG 300
 gagTGTGAcG atgCTGCCAC ttACTATTGt caACAGGGTT attCTATCAG tGATATTGAT 360
 aatgCTTcG gCGGAGGGAC CGAGGTGGTg gtCAAAGGTG atCCAGTTGc acCTACTGTC 420
 ctCCtCTTCC caccatCTAG cgATGAGGTG gCAACTGGAA cAGTCACCAT cGTGTGTG 480
 gCGAATAAAAT acTTTCCGA tGTCACCgTC acCTGGGAGG tGGATGGCAC cacCCAAACA 540
 actGGCATCG agAACAGTAA AACACCGCAG aATTCTGCAG attGTACCTA caACCTCAGC 600
 agCActCTGA cACTGACCGAG CACACAGTAC AACAGCCACA aAGAGTACAC CTGCAAGGTG 660
 accCAGGGCA CGACCTCAGT CGTCCAGAGC tTCAGTAGGA agAACTGTTA a 711

<210> 64
 <211> 459
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic M83 006G05L heavy chain sequence

<400> 64
 Met Glu Thr Gly Leu Arg Trp Leu Leu Val Ala Val Leu Lys Gly
 1 5 10 15
 Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Ser Pro
 20 25 30
 Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Leu Ser
 35 40 45
 Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 50 55 60
 Tyr Ile Gly Ile Ile Ser Ser Ser Gly Ser Thr Tyr Tyr Ala Ser Trp
 65 70 75 80
 Ala Lys Gly Arg Phe Thr Ile Ser Lys Thr Ser Thr Thr Val Asp Leu
 85 90 95
 Glu Val Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ser
 100 105 110
 Arg Glu His Ala Gly Tyr Ser Gly Asp Thr Gly His Leu Trp Gly Pro
 115 120 125

Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val
130					135					140					
Phe	Pro	Leu	Ala	Pro	Cys	Cys	Gly	Asp	Thr	Pro	Ser	Ser	Thr	Val	Thr
145					150				155						160
Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Leu	Pro	Glu	Pro	Val	Thr	Val	Thr
					165			170						175	
Trp	Asn	Ser	Gly	Thr	Leu	Thr	Asn	Gly	Val	Arg	Thr	Phe	Pro	Ser	Val
					180			185			190				
Arg	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Ser	Val	Thr
					195			200			205				
Ser	Ser	Ser	Gln	Pro	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala	Thr	Asn
					210			215			220				
Thr	Lys	Val	Asp	Lys	Thr	Val	Ala	Pro	Ser	Thr	Cys	Ser	Lys	Pro	Thr
					225			230			235			240	
Cys	Pro	Pro	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Ile	Phe	Pro
					245			250			255				
Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr
					260			265			270				
Cys	Val	Val	Val	Asp	Val	Ser	Gln	Asp	Asp	Pro	Glu	Val	Gln	Phe	Thr
					275			280			285				
Trp	Tyr	Ile	Asn	Asn	Glu	Gln	Val	Arg	Thr	Ala	Arg	Pro	Pro	Leu	Arg
					290			295			300				
Glu	Gln	Gln	Phe	Asn	Ser	Thr	Ile	Arg	Val	Val	Ser	Thr	Leu	Pro	Ile
					305			310			315			320	
Ala	His	Gln	Asp	Trp	Leu	Arg	Gly	Lys	Glu	Phe	Lys	Cys	Lys	Val	His
					325			330			335				
Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Arg
					340			345			350				
Gly	Gln	Pro	Leu	Glu	Pro	Lys	Val	Tyr	Thr	Met	Gly	Pro	Pro	Arg	Glu
					355			360			365				
Glu	Leu	Ser	Ser	Arg	Ser	Val	Ser	Leu	Thr	Cys	Met	Ile	Asn	Gly	Phe
					370			375			380				
Tyr	Pro	Ser	Asp	Ile	Ser	Val	Glu	Trp	Glu	Lys	Asn	Gly	Lys	Ala	Glu
					385			390			395			400	
Asp	Asn	Tyr	Lys	Thr	Thr	Pro	Ala	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr
					405			410			415				
Phe	Leu	Tyr	Asn	Lys	Leu	Ser	Val	Pro	Thr	Ser	Glu	Trp	Gln	Arg	Gly
					420			425			430				
Asp	Val	Phe	Thr	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr
					435			440			445				
Thr	Gln	Lys	Ser	Ile	Ser	Arg	Ser	Pro	Gly	Lys					
					450			455							

<210> 65
<211> 1377
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic M83 006G05L anti-CD83 heavy chain sequence

<400> 65
atggagacag gcctgcgctg gcttctcctg gtcgctgtgc tcaaagggtgt ccagtgtcag 60
tcgggtggagg agtccggggg tcgcctggc tcgcctggga caccctgac actcacctgc 120
acagcctctg gattctccct cagtagctac gacatgagct gggtccggca ggctccaggg 180
aaggggctgg aatacatcggt aatcattttt agtagtggtt gcacatacta cgcgagctgg 240
gcaaaaggcc gattcaccat ctccaaaacc tcgaccacgg tggatctggaa agtgaccagt 300
ctgacaaccg aggacacggc caccttatttc tgttagtagag aacatgctgg ttatagtgg 360
gatacgggtc acttgtgggg cccaggcacc ctggtcaccg tctcctcgaa gcaacctaag 420

gctccatcg tcttcccact	ggccccctgc	tgcggggaca	caccctctag	cacggtgacc	480
ttgggctgcc	tggtaaaagg	ctacctcccg	gaggcagtga	ccgtgacctg	540
accctcacca	atgggtacg	caccccccgg	tccgtccggc	agtcctcagg	600
ctgagcagcg	tggtgagcgt	gacctaagc	agccagcccg	tcacctgaa	660
ccagccacca	acaccaaagt	ggacaagacc	gttgcgcct	cgacatgcag	720
tgcccacccc	ctgaactcct	ggggggacgg	tctgtcttca	tcttcccccc	780
gacaccctca	tgatctcagc	caccccccgg	gtcacatgcg	tgggtgttga	840
gatgaccccg	aggtgcagtt	cacatggta	ataaacaacg	agcaggtgcg	900
ccggccgtac	gggagcagca	gttcaacacg	acgatcccg	tggtcagcac	960
ggcaccagg	actggctgag	gggcaaggag	ttcaagtgc	aagtccacaa	1020
ccggccccca	tcgagaaaac	catctccaaa	gccagagggc	caaggcactc	1080
tacaccatgg	gcccctcccg	ggaggagctg	agcagcaggt	cggtcagcct	1140
atcaacggct	tctacccttc	cgacatctcg	gtggagtggg	gacatgcac	1200
gacaactaca	agaccacg	gcccgtgtc	gacagcgc	gttcctactc	1260
aagctctcag	tgcccacgag	tgagtggcag	cggggcgcacg	tcttcacctg	1320
cacgaggcct	tgcacaacca	ctacacgcac	aagtccatct	ctccgtgtatg	1377
				gggtaaa	

<210> 66
<211> 150
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 heavy chain variable region sequence

<400> 66

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5				10					15		
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
								20				25		30	
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Phe	Thr	Ile	Ser
								35				40		45	
Asp	Tyr	Asp	Leu	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Glu	Gly	Leu	Lys
								50			55		60		
Tyr	Ile	Gly	Phe	Ile	Ala	Ile	Asp	Gly	Asn	Pro	Tyr	Tyr	Ala	Thr	Trp
								65			70		75		80
Ala	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Lys	Thr	Ser	Thr	Thr	Val	Asp	Leu
								85			90		95		
Lys	Ile	Thr	Ala	Pro	Thr	Thr	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys	Ala
								100			105		110		
Arg	Gly	Ala	Gly	Asp	Leu	Trp	Gly	Pro	Gly	Thr	Leu	Val	Thr	Val	Ser
								115			120		125		
Ser	Gly	Gln	Pro	Lys	Ala	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Cys
								130			135		140		
Gly	Asp	Thr	Pro	Ser	Ser										
								145			150				

<210> 67
<211> 152
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic anti-CD83 heavy chain variable region sequence

<400> 67

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5				10					15		
Val	His	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
								20				25		30	

Gly Thr Pro Leu Thr Leu Thr Cys Thr Ala Ser Gly Phe Ser Arg Ser
 35 40 45
 Ser Tyr Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
 50 55 60
 Trp Val Gly Val Ile Ser Thr Ala Tyr Asn Ser His Tyr Ala Ser Trp
 65 70 75 80
 Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu
 85 90 95
 Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala
 100 105 110
 Arg Gly Gly Ser Trp Leu Asp Leu Trp Gly Gln Gly Thr Leu Val Thr
 115 120 125
 Val Ser Ser Gly Gln Pro Lys Ala Pro Ser Val Phe Pro Leu Ala Pro
 130 135 140
 Cys Cys Gly Asp Thr Pro Ser Ser
 145 150

<210> 68
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A synthetic anti-CD83 light chain variable region
 sequence

<400> 68
 Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
 1 5 10 15
 Leu Pro Gly Ala Arg Cys Ala Asp Val Val Met Thr Gln Thr Pro Ala
 20 25 30
 Ser Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser
 35 40 45
 Ser Lys Asn Val Tyr Asn Asn Asn Trp Leu Ser Trp Phe Gln Gln Lys
 50 55 60
 Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala
 65 70 75 80
 Ser Gly Val Pro Ser Arg Phe Arg Gly Ser Gly Ser Gly Thr Gln Phe
 85 90 95
 Thr Leu Thr Ile Ser Asp Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr
 100 105 110
 Cys Ala Gly Asp Tyr Ser Ser Ser Asp Asn Gly Phe Gly Gly Gly
 115 120 125
 Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu
 130 135 140
 Phe Pro Pro Ser Ser
 145

<210> 69
 <211> 149
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SITE
 <222> (1)...(149)
 <223> Xaa = any amino acid

<220>
 <223> A synthetic anti-CD83 light chain variable region
 sequence

<400> 69
Met Asp Xaa Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Arg Cys Ala Leu Val Met Thr Gln Thr Pro Ala Ser
20 25 30
Val Ser Ala Ala Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
35 40 45
Gln Ser Val Tyr Asp Asn Asp Glu Leu Ser Trp Tyr Gln Gln Lys Pro
50 55 60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Leu Ala Ser Lys Leu Ala Ser
65 70 75 80
Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Ala
85 90 95
Leu Thr Ile Ser Gly Val Gln Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
100 105 110
Gln Ala Thr His Tyr Ser Ser Asp Trp Tyr Leu Thr Phe Gly Gly Gly
115 120 125
Thr Glu Val Val Val Lys Gly Asp Pro Val Ala Pro Thr Val Leu Leu
130 135 140
Phe Pro Pro Ser Ser
145

<210> 70
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic 96G08 light chain sequence

<400> 70
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Thr Phe Ala Gln Val Leu Thr Gln Thr Ala Ser Pro
20 25 30
Val Ser Ala Pro Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser Ser
35 40 45
Gln Ser Val Tyr Asn Asn Asp Phe Leu Ser Trp Tyr Gln Gln Lys Pro
50 55 60
Gly Gln Pro Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Ala Ser
65 70 75 80
Gly Val Pro Ser Arg Phe Lys Gly Ser Gly Ser Gly Thr Gln Phe Thr
85 90 95
Leu Thr Ile Ser Asp Leu Glu Cys Asp Asp Ala Ala Thr Tyr Tyr Cys
100 105 110
Thr Gly Thr Tyr Gly Asn Ser Ala Trp Tyr Glu Asp Ala Phe Gly Gly
115 120 125
Gly Thr Glu Val Val Val Lys Arg Thr Pro Val Ala Pro Thr Val Leu
130 135 140
Leu Phe Pro Pro Ser Ser Ala Glu Leu Ala Thr Gly Thr Ala Thr Ile
145 150 155 160
Val Cys Val Ala Asn Lys Tyr Phe Pro Asp Gly Thr Val Thr Trp Lys
165 170 175
Val Asp Gly Ile Thr Gln Ser Ser Gly Ile Asn Asn Ser Arg Thr Pro
180 185 190
Gln Asn Ser Ala Asp Cys Thr Tyr Asn Leu Ser Ser Thr Leu Thr Leu
195 200 205
Ser Ser Asp Glu Tyr Asn Ser His Asp Glu Tyr Thr Cys Gln Val Ala
210 215 220
Gln Asp Ser Gly Ser Pro Val Val Gln Ser Phe Ser Arg Lys Ser Cys
225 230 235 240

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<210> 71
<211> 13
<212> PRT
<213> Oryctolagus cuniculus

<400> 71
Gln Ser Ser Gln Ser Val Tyr Asn Asn Asp Phe Leu Ser
1 5 10

<210> 72
<211> 7
<212> PRT
<213> Oryctolagus cuniculus

<400> 72
Tyr Ala Ser Thr Leu Ala Ser
1 5

<210> 73
<211> 13
<212> PRT
<213> Oryctolagus cuniculus

<400> 73
Thr Gly Thr Tyr Gly Asn Ser Ala Trp Tyr Glu Asp Ala
1 5 10

<210> 74
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> A synthetic 96G08 anti-CD83 light chain sequence

<400> 74
atggacacga gggcccccac tcagctgctg gggctcctgc tgctctggct cccaggtgcc 60
acatttgcgc aagtgcgtac ccagactgca tcgcccgtgt ctgcacctgt gggaggcaca 120
gtcaccatca attgccagtc cagtcagagt gtttataata acgacttctt atcctggtat 180
cagcagaaac cagggcagcc tcccaaactc ctgatctatt atgcatccac tctggcatct 240
gggttcccat ccccggttcaa aggcaagtggta tctggacac agttcaactt caccatcagc 300
gacctggagt gtgacgatgc tgccacttac tactgtacag gcacttatgg taatagtgtct 360
tggtacgagg atgcatttcgg cggagggacc gaggtgggtgg tcaaacgtac gccagttgca 420
cctactgtcc tcctcttccc accatcttagc gctgagctgg caactggAAC agccaccatc 480
gtgtgcgtgg cgaataaaata ctttcccgat ggcacccgtca cctggaaaggt ggatggcatc 540
acccaaagca gcggcatcaa taacagtaga acaccgcaga attctgcaga ttgtacctac 600
aacctcagca gtactctgac actgagcagc gacgagtaca acagccacga cgagtacacc 660
tgccaggtgg cccaggactc aggctcaccc gtcgtccaga gttcagtag gaagagctgt 720
tag 723

<210> 75
<211> 25
<212> DNA
<213> Oryctolagus cuniculus

<400> 75
cagtccagtc agagtgttta taata 25

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<210> 76		
<211> 20		
<212> DNA		
<213> Oryctolagus cuniculus		
<400> 76		
atgcatccac tctggcatct		20
<210> 77		
<211> 25		
<212> DNA		
<213> Oryctolagus cuniculus		
<400> 77		
acaggcaact atggtaatag tgctt		25
<210> 78		
<211> 456		
<212> PRT		
<213> Artificial Sequence		
<220>		
<223> A synthetic 96G08 heavy chain sequence		
<400> 78		
Met Glu Thr Gly Leu Arg Trp Leu Leu Leu Val Ala Val Leu Lys Gly		
1 5 10 15		
Val Gln Cys Gln Ser Val Glu Glu Ser Gly Gly Arg Leu Val Thr Pro		
20 25 30		
Gly Thr Pro Leu Thr Leu Thr Cys Thr Val Ser Gly Ile Asp Leu Ser		
35 40 45		
Ser Asp Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu		
50 55 60		
Trp Ile Gly Ile Ile Ser Ser Gly Gly Asn Thr Tyr Tyr Ala Ser Trp		
65 70 75 80		
Ala Lys Gly Arg Phe Thr Ile Ser Arg Thr Ser Thr Thr Val Asp Leu		
85 90 95		
Lys Met Thr Ser Leu Thr Thr Glu Asp Thr Ala Thr Tyr Phe Cys Ala		
100 105 110		
Arg Val Val Gly Gly Thr Tyr Ser Ile Trp Gly Gln Gly Thr Leu Val		
115 120 125		
Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Tyr Pro Leu Ala		
130 135 140		
Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu		
145 150 155 160		
Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly		
165 170 175		
Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp		
180 185 190		
Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro		
195 200 205		
Ser Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys		
210 215 220		
Val Asp Lys Lys Ile Val Pro Arg Asp Cys Gly Cys Lys Pro Cys Ile		
225 230 235 240		
Cys Thr Val Pro Glu Val Ser Ser Val Phe Ile Phe Pro Pro Lys Pro		
245 250 255		
Lys Asp Val Leu Thr Ile Thr Leu Thr Pro Lys Val Thr Cys Val Val		
260 265 270		
Val Asp Ile Ser Lys Asp Asp Pro Glu Val Gln Phe Ser Trp Phe Val		
275 280 285		

Asp Asp Val Glu Val His Thr Ala Gln Thr Gln Pro Arg Glu Glu Gln
 290 295 300
 Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro Ile Met His Gln
 305 310 315 320
 Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val Asn Ser Ala Ala
 325 330 335
 Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Arg Pro
 340 345 350
 Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys Glu Gln Met Ala
 355 360 365
 Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp Phe Phe Pro Glu
 370 375 380
 Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro Ala Glu Asn Tyr
 385 390 395 400
 Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser Tyr Phe Val Tyr
 405 410 415
 Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala Gly Asn Thr Phe
 420 425 430
 Thr Cys Ser Val Leu His Glu Gly Leu His Asn His His Thr Glu Lys
 435 440 445
 Ser Leu Ser His Ser Pro Gly Lys
 450 455

<210> 79
 <211> 5
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 79
 Ser Asp Gly Ile Ser
 1 5

<210> 80
 <211> 16
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 80
 Ile Ile Ser Ser Gly Gly Asn Thr Tyr Tyr Ala Ser Trp Ala Lys Gly
 1 5 10 15

<210> 81
 <211> 8
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 81
 Val Val Gly Gly Thr Tyr Ser Ile
 1 5

<210> 82
 <211> 1371
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 96G08 anti-CD83 heavy chain sequence

<400> 82
 atggagactg ggctgcgctg gcttctcctg gtcgctgtgc tcaaagggtgt ccagtgtcag 60
 tcggtgagg agtccggggg tcgcctggtc acacctggga caccctgac actcacctgc 120

acagtgtctg	aatcgacct	cagtagcgat	ggaataagct	gggtccggca	ggctccaggg	180
aaggggctgg	aatggatcg	aatcattagt	agtgtggta	acacatacta	cgcgagctgg	240
gcaaaaaggc	gattcacat	ctccagaacc	tcgaccacgg	tggatctgaa	gatgaccagt	300
ctgacaaccg	aggacacggc	cacctatttc	tgtgccagag	ttgttggtg	tacttatagc	360
atctggggcc	agggcaccct	cgtcaccgtc	tcgagcgctt	ctacaaaggg	cccatctgtc	420
tatccactgg	cccctggatc	tgctgccccaa	actaactcca	ttgtgaccct	ggatgcctg	480
gtcaaggggct	atttcctga	gccagtgaca	gtgacctgga	actctggatc	cctgtccagc	540
ggtgtgcaca	ccttcccagc	tgtcctgcag	tctgacctct	acactctgag	cagtcagtg	600
actgtcccct	ccagcacctg	gcccgccag	accgtcacct	gcaacgtgc	ccacccggcc	660
agcagcacca	aggtggacaa	aaaaattgtg	cccaggatt	gtggttgtaa	gccttgcata	720
tgtagcgtcc	cagaagtatac	atctgtctc	atctcccccc	caaagccaa	ggatgtgtc	780
accattactc	tgactcctaa	gtcacgtgt	gttgggttag	acatcagaa	ggatgtatcc	840
gaggtccagt	tcagctggtt	tgtagatgat	gtggagggtgc	acacagctca	gacgcaaccc	900
cgggaggaggc	agttcaaacag	cacttccgc	tcagtcagtg	aacttcccat	catgcaccag	960
gactggctca	atggcaagga	gttcaaatgc	agggtcaaca	gtgcagctt	ccctgcccccc	1020
atcgagaaaa	ccatctccaa	accCAAAGC	agaccgaagg	ctccacaggt	gtacaccatt	1080
ccacctccca	aggagcagat	gcccaaggat	aaagtca	tgacctgcac	gataacagac	1140
ttcttccctg	aagacattac	tgtggagtt	cagtggatg	ggcagccagc	ggagaactac	1200
aagaacactc	agcccatcat	ggacacagat	ggctcttact	tcgtctacag	caagctcaat	1260
gtcagaaga	gcaactggga	gcccggaaat	acttcacct	gctctgtgtt	acatgagggc	1320
ctgcacaacc	accatactga	gaagagcctc	tcccactctc	ctggtaatg	a	1371

<210> 83
<211> 15
<212> DNA
<213> Oryctolagus cuniculus

<400> 83
agcgatggaa taagc 15

<210> 84
<211> 48
<212> DNA
<213> Oryctolagus cuniculus

<400> 84
atcattagta gtgggtgtaa cacatactac gcgagctggg caaaaggc 48

<210> 85
<211> 24
<212> DNA
<213> Oryctolagus cuniculus

<400> 85
gttgggtg gtacttatac catc 24

<210> 86
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> A synthetic 95F04 light chain sequence

<400> 86
Met Asp Thr Arg Ala Pro Thr Gln Leu Leu Gly Leu Leu Leu Trp
1 5 10 15
Leu Pro Gly Ala Thr Phe Ala Gln Ala Val Val Thr Gln Thr Thr Ser
20 25 30
Pro Val Ser Ala Pro Val Gly Gly Thr Val Thr Ile Asn Cys Gln Ser
35 40 45

Ser	Gln	Ser	Val	Tyr	Gly	Asn	Asn	Glu	Leu	Ser	Trp	Tyr	Gln	Gln	Lys
50						55					60				
Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Gln	Ala	Ser	Ser	Leu	Ala
65					70					75				80	
Ser	Gly	Val	Pro	Ser	Arg	Phe	Lys	Gly	Ser	Gly	Ser	Gly	Thr	Gln	Phe
						85			90				95		
Thr	Leu	Thr	Ile	Ser	Asp	Leu	Glu	Cys	Asp	Asp	Ala	Ala	Thr	Tyr	Tyr
						100			105				110		
Cys	Leu	Gly	Glu	Tyr	Ser	Ile	Ser	Ala	Asp	Asn	His	Phe	Gly	Gly	Gly
						115			120				125		
Thr	Glu	Val	Val	Val	Lys	Arg	Thr	Pro	Val	Ala	Pro	Thr	Val	Leu	Leu
						130			135				140		
Phe	Pro	Pro	Ser	Ser	Ala	Glu	Leu	Ala	Thr	Gly	Thr	Ala	Thr	Ile	Val
145						150				155				160	
Cys	Val	Ala	Asn	Lys	Tyr	Phe	Pro	Asp	Gly	Thr	Val	Thr	Trp	Lys	Val
						165			170				175		
Asp	Gly	Ile	Thr	Gln	Ser	Ser	Gly	Ile	Asn	Asn	Ser	Arg	Thr	Pro	Gln
						180			185				190		
Asn	Ser	Ala	Asp	Cys	Thr	Tyr	Asn	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser
						195			200				205		
Ser	Asp	Glu	Tyr	Asn	Ser	His	Asp	Glu	Tyr	Thr	Cys	Gln	Val	Ala	Gln
						210			215				220		
Asp	Ser	Gly	Ser	Pro	Val	Val	Gln	Ser	Phe	Ser	Arg	Lys	Ser	Cys	
						225			230				235		

<210> 87

<211> 13

<212> PRT

<213> Oryctolagus cuniculus

<400> 87

Gln	Ser	Ser	Gln	Ser	Val	Tyr	Gly	Asn	Asn	Glu	Leu	Ser
1					5					10		

<210> 88

<211> 7

<212> PRT

<213> Oryctolagus cuniculus

<400> 88

Gln	Ala	Ser	Ser	Leu	Ala	Ser
1				5		

<210> 89

<211> 11

<212> PRT

<213> Oryctolagus cuniculus

<400> 89

Leu	Gly	Glu	Tyr	Ser	Ile	Ser	Ala	Asp	Asn	His
1					5					10

<210> 90

<211> 720

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic 95F04 anti-CD83 light chain sequence

<400> 90															
atggacacga	gggcccccac	ttagctgctg	gggctcctgc	tgctctggct	cccaggtgcc	60									
acatttgc	ccaa	aaggcggt	gacc	caga	act	atcgcccg	tgtctgc	acc	tgtgggaggc	120					
acagtca	cca	tcaattg	cca	gtcc	cagt	ca	agt	tttat	gtaaca	acga	attatc	cctgg	180		
tatc	cagc	aga	aacc	aggc	ca	gc	ctc	ctgat	acc	aggc	atc	cagc	ctgg	240	
tct	gggg	tcc	catc	cggt	tt	caa	aggc	agt	atc	gg	atc	tct	accatc	300	
agc	gac	ctgg	gg	actg	tg	tg	tc	tg	act	gt	tc	tc	accat	360	
gct	gata	atc	tt	tcgg	gg	gg	gg	gg	tt	gg	ca	ta	tt	tt	
act	gtc	c	tc	ttccc	acc	atc	tag	tcg	tc	gg	aa	cc	atc	gtg	420
tgc	gtgg	cg	ga	ataa	actt	tccc	gat	g	cc	gt	cc	at	cc	cc	480
caa	aggc	cg	cg	cat	caataa	cag	taga	a	cc	ca	cc	at	cc	cc	540
ctc	agc	gt	gt	act	ct	ct	gac	act	g	g	g	ac	cc	cc	600
cag	gt	gg	cc	agg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	660
cag	gt	gg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	720

<210> 91

<211> 460

<212> PRT

<213> Artificial Sequence

<220>

<223> A synthetic 95F04 heavy chain sequence

<400> 91

Met	Glu	Thr	Gly	Leu	Arg	Trp	Leu	Leu	Leu	Val	Ala	Val	Leu	Lys	Gly
1				5				10					15		
Val	Gln	Cys	Gln	Ser	Val	Glu	Glu	Ser	Gly	Gly	Arg	Leu	Val	Thr	Pro
					20			25					30		
Gly	Thr	Pro	Leu	Thr	Leu	Thr	Cys	Thr	Val	Ser	Gly	Ile	Asp	Leu	Ser
					35			40				45			
Ser	Asn	Ala	Met	Ile	Trp	Val	Arg	Gln	Ala	Pro	Arg	Glu	Gly	Leu	Glu
					50			55				60			
Trp	Ile	Gly	Ala	Met	Asp	Ser	Asn	Ser	Arg	Thr	Tyr	Tyr	Ala	Thr	Trp
					65			70			75		80		
Ala	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Thr	Ser	Ser	Ile	Thr	Val	Asp
					85			90				95			
Leu	Lys	Ile	Thr	Ser	Pro	Thr	Thr	Glu	Asp	Thr	Ala	Thr	Tyr	Phe	Cys
					100			105				110			
Ala	Arg	Gly	Asp	Gly	Gly	Ser	Ser	Asp	Tyr	Thr	Glu	Met	Trp	Gly	Pro
					115			120				125			
Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val
					130			135			140				
Tyr	Pro	Leu	Ala	Pro	Gly	Ser	Ala	Ala	Gln	Thr	Asn	Ser	Met	Val	Thr
					145			150			155		160		
Leu	Gly	Cys	Leu	Val	Lys	Gly	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Thr
					165			170				175			
Trp	Asn	Ser	Gly	Ser	Leu	Ser	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val
					180			185			190				
Leu	Gln	Ser	Asp	Leu	Tyr	Thr	Leu	Ser	Ser	Ser	Val	Thr	Val	Pro	Ser
					195			200			205				
Ser	Thr	Trp	Pro	Ser	Glu	Thr	Val	Thr	Cys	Asn	Val	Ala	His	Pro	Ala
					210			215			220				
Ser	Ser	Thr	Lys	Val	Asp	Lys	Lys	Ile	Val	Pro	Arg	Asp	Cys	Gly	Cys
					225			230			235		240		
Lys	Pro	Cys	Ile	Cys	Thr	Val	Pro	Glu	Val	Ser	Ser	Val	Phe	Ile	Phe
					245			250				255			
Pro	Pro	Lys	Pro	Lys	Asp	Val	Leu	Thr	Ile	Thr	Leu	Thr	Pro	Lys	Val
					260			265			270				
Thr	Cys	Val	Val	Val	Asp	Ile	Ser	Lys	Asp	Asp	Pro	Glu	Val	Gln	Phe
					275			280			285				
Ser	Trp	Phe	Val	Asp	Asp	Val	Glu	Val	His	Thr	Ala	Gln	Thr	Gln	Pro
					290			295			300				

Arg Glu Glu Gln Phe Asn Ser Thr Phe Arg Ser Val Ser Glu Leu Pro
 305 310 315 320
 Ile Met His Gln Asp Trp Leu Asn Gly Lys Glu Phe Lys Cys Arg Val
 325 330 335
 Asn Ser Ala Ala Phe Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr
 340 345 350
 Lys Gly Arg Pro Lys Ala Pro Gln Val Tyr Thr Ile Pro Pro Pro Lys
 355 360 365
 Glu Gln Met Ala Lys Asp Lys Val Ser Leu Thr Cys Met Ile Thr Asp
 370 375 380
 Phe Phe Pro Glu Asp Ile Thr Val Glu Trp Gln Trp Asn Gly Gln Pro
 385 390 395 400
 Ala Glu Asn Tyr Lys Asn Thr Gln Pro Ile Met Asp Thr Asp Gly Ser
 405 410 415
 Tyr Phe Val Tyr Ser Lys Leu Asn Val Gln Lys Ser Asn Trp Glu Ala
 420 425 430
 Gly Asn Thr Phe Thr Cys Ser Val Leu His Glu Gly Leu His Asn His
 435 440 445
 His Thr Glu Lys Ser Leu Ser His Ser Pro Gly Lys
 450 455 460

<210> 92
 <211> 5
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 92
 Ser Asn Ala Met Ile
 1 5

<210> 93
 <211> 16
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 93
 Ala Met Asp Ser Asn Ser Arg Thr Tyr Tyr Ala Thr Trp Ala Lys Gly
 1 5 10 15

<210> 94
 <211> 11
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 94
 Gly Asp Gly Gly Ser Ser Asp Tyr Thr Glu Met
 1 5 10

<210> 95
 <211> 1383
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 95F04 anti-CD83 heavy chain sequence

<400> 95
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 tcggtgagg agtccgggg tcgcctggc acgcctggg caccctgac actcacctgc 120
 acagtctctg gaatcgacct cagtagcaat gcaatgatct gggccgcga ggctccaagg 180
 gaggggctgg aatggatcgg agccatggat agtaatagta ggacgtacta cgcgacctgg 240
 gcgaaaggcc gattcaccat ctccagaacc tcgtcgatta cggtgatct gaaaatcacc 300

agtccgacaa	ccgaggacac	ggcccacatat	ttctgtgcca	gagggatgg	tggcagtagt	360
gattatacag	agatgtgggg	cccaggacc	ctcgaccc	tctcgagcgc	ttctacaaag	420
ggcccatctg	tctatccact	ggccccctgga	tctgtgccc	aaactaactc	catggtgacc	480
ctggatgccc	tggtaagggg	ctatccc	gagccagtga	cagtgaccc	gaactctgga	540
tccctgtcca	gcgggtgtca	caccccca	gctgtcctgc	agtctgaccc	ctacactctg	600
agcagtcag	tgactgtccc	ctccagcacc	tggcccagcg	agaccgtcac	ctgcaacgtt	660
gcccacccgg	ccagcagcac	caaggtggac	aagaaaattt	tgcccaggg	ttgtgggtt	720
aaggcttgc	tatgtacagt	cccagaagta	tcatctgtct	tcatcttccc	cccaaagccc	780
aaggatgtgc	tcaccattac	tctgactctt	aaggtcacgt	gtgttgtgtt	agacatcagc	840
aaggatgatc	ccgaggtcca	gttcagctgg	ttttagatg	atgtggaggt	gcacacagct	900
cagacgcaac	cccggggg	gcagttcaac	agcactttcc	gctcagtcag	tgaacttccc	960
atcatgcacc	aggactggct	caatggcaag	gagttcaaat	gcagggtcaa	cagtgcagct	1020
ttccctgccc	ccatcgagaa	aaccatctcc	aaaacccaaag	gcagaccgaa	ggctccacag	1080
gtgtacacca	ttccacactcc	caaggagcag	atggcaagg	ataaaagtca	tctgacctgc	1140
atgataacag	acttcttccc	tgaagacatt	actgtggagt	ggcagtgaa	tggcagcca	1200
gcccggaaact	acaagaacac	tcagcccatc	atggacacag	atggcttta	cttcgtctac	1260
agcaagctca	atgtgcagaa	gagcaactgg	gaggcaggaa	atactttcac	ctgctctgt	1320
ttacatgagg	gcctgcacaa	ccaccatact	gagaagagcc	tctcccactc	tcctggtaaa	1380
	tga					1383

<210> 96

<211> 1383

<212> DNA

<213> Artificial Sequence

<220>

<223> A synthetic 95F04 anti-CD83 light chain sequence

<400> 96

atggagactg	ggctgcgctg	gttctccctg	gtcgctgtgc	tcaaagggtgt	ccagtgtcag	60
tcgggggg	agtccccccc	tgcctggc	acgcctggg	caccctgtac	actcacctgc	120
acagtctcg	gaatcgacct	cagtagcaat	gcaatgatct	gggtccggca	ggctccaagg	180
gaggggctgg	aatggatcgg	agccatggat	agtaatagta	ggacgtacta	cgcgacctgg	240
gcgaaaggcc	gattcaccat	ctccagaacc	tcgtcgat	cgggtggatct	gaaaatcacc	300
atccgacaa	ccgaggacac	ggccacat	ttctgtgcca	gaggggatgg	tggcagtagt	360
gattatacag	agatgtgggg	cccaggacc	ctcgaccc	tctcgagcgc	ttctacaaag	420
ggcccatctg	tctatccact	ggccccctgga	tctgtgccc	aaactaactc	catggtgacc	480
ctggatgccc	tggtaagggg	ctatccc	gagccagtga	cagtgaccc	gaactctgga	540
tccctgtcca	gcgggtgtca	caccccca	gctgtcctgc	agtctgaccc	ctacactctg	600
agcagtcag	tgactgtccc	ctccagcacc	tggccagcg	agaccgtcac	ctgcaacgtt	660
gcccacccgg	ccagcagcac	caaggtggac	aagaaaattt	tgcccaggg	ttgtgggtt	720
aaggcttgc	tatgtacagt	cccagaagta	tcatctgtct	tcatcttccc	cccaaagccc	780
aaggatgtgc	tcaccattac	tctgactctt	aaggtcacgt	gtgttgtgtt	agacatcagc	840
aaggatgatc	ccgaggtcca	gttcagctgg	ttttagatg	atgtggaggt	gcacacagct	900
cagacgcaac	cccggggg	gcagttcaac	agcactttcc	gctcagtcag	tgaacttccc	960
atcatgcacc	aggactggct	caatggcaag	gagttcaaat	gcagggtcaa	cagtgcagct	1020
ttccctgccc	ccatcgagaa	aaccatctcc	aaaacccaaag	gcagaccgaa	ggctccacag	1080
gtgtacacca	ttccacactcc	caaggagcag	atggcaagg	ataaaagtca	tctgacctgc	1140
atgataacag	acttcttccc	tgaagacatt	actgtggagt	ggcagtgaa	tggcagcca	1200
gcccggaaact	acaagaacac	tcagcccatc	atggacacag	atggcttta	cttcgtctac	1260
agcaagctca	atgtgcagaa	gagcaactgg	gaggcaggaa	atactttcac	ctgctctgt	1320
ttacatgagg	gcctgcacaa	ccaccatact	gagaagagcc	tctcccactc	tcctggtaaa	1380
	tga					1383

<210> 97

<211> 107

<212> PRT

<213> Homo sapiens

<400> 97

Pro Glu Val Lys Val Ala Cys Ser Glu Asp Val Asp Leu Pro Cys Thr

1

5

10

15

Ala Pro Trp Asp Pro Gln Val Pro Tyr Thr Val Ser Trp Val Lys Leu
 20 25 30
 Leu Glu Gly Gly Glu Glu Arg Met Glu Thr Pro Gln Glu Asp His Leu
 35 40 45
 Arg Gly Gln His Tyr His Gln Lys Gly Gln Asn Gly Ser Phe Asp Ala
 50 55 60
 Pro Asn Glu Arg Pro Tyr Ser Leu Lys Ile Arg Asn Thr Thr Ser Cys
 65 70 75 80
 Asn Ser Gly Thr Tyr Arg Cys Thr Leu Gln Asp Pro Asp Gly Gln Arg
 85 90 95
 Asn Leu Ser Gly Lys Val Ile Leu Arg Val Thr
 100 105

<210> 98
 <211> 8
 <212> PRT
 <213> Oryctolagus cuniculus

<400> 98
 Gln Ser Val Tyr Asp Asn Asp Glu
 1 5

<210> 99
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> A synthetic 96G08 anti-CD83 light chain sequence

<400> 99
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 acatttgcgc aagtgtgac ccagactgca tcgcccgtgt ctgcacctgt gggaggcaca 120
 gtcaccatca attgccagtc cagttagt gtttataata acgacttctt atcctggtat 180
 cagcagaaac cagggcagcc tcccaaactc ctgatctatt atgcattcac tctggcatct 240
 ggggtccccat ccccggttcaa aggcatgtga tctggacac agttcactct caccatcagc 300
 gacctggagt gtgacgatgc gccacttact actgtacagg cacttatggt aatagtgttt 360
 ggtacgagga tgcttcggc ggagggaccc aggtgggtggt caaacgtacg ccagttgcac 420
 ctactgtcct cctcttccca ccatctagcg ctgagctggc aactggaaaca gccaccatcg 480
 tgtgcgtggc gaataaatac ttcccgtat gcaccgtcac ctggaagggtg gatggcatca 540
 cccaaagcag cggcatcaat aacagttagaa caccgcagaa ttctgcagat tgtacctaca 600
 acctcagcag tactctgaca ctgagcagcg acgagttacaa cagccacgac gagtacacct 660
 gccaggtggc ccaggactca ggctcaccgg tcgtccagag cttcagtagg aagagctgtt 720